Serial No: 10/716.330 Filed: November 18, 2003 WSGR Reference No. 34569-704.201

Amendment to the Abstract

Please replace the Abstract as follows:

Embodiments of this invention include application of new inferential methods to analysis of complex biological information, including gene networks. In some embodiments, time course data obtained simultaneously for a number of genes in an organism. New methods include modifications of Bayesian inferential methods and application of those methods to determining cause and effect relationships between expressed genes, and in some embodiments, for determining upstream effectors of regulated genes. Additional modifications of Bayesian methods include use of time course data to infer causal relationships between expressed genes. Other embodiments include the use of bootstrapping methods and determination of edge effects to more accurately provide network information between expressed genes. Information about gene networks can be stored in a memory device and can be transmitted to an output device, or can be transmitted to remote location.

Methods are provided for constructing a gene network of relationships between genes and generating a relationships graph. Methods may include providing a quantitative time course data library including expression results including gene expression data at time points. Methods may comprise quantifying an average effect on expression of each gene by each other gene and quantifying variability. Methods may comprise creating a gene expression matrix including matrix data of effects. Methods may include applying a Bayesian computational model to the matrix data. The Bayesian model includes minimizing a BNRC_{dynamic} criterion. Methods may include generating the gene network and generating a gene network graph. Methods are provided for constructing a gene network model from time course gene expression data and applying a Bayesian computational model to the data. Methods may include generating a graph of the gene network model from applying the Bayesian model where BNRC dynamic criterion is minimized.